



PCT10

RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/10/019,541

TIME: 17:07:35

Input*Set : A:\019541

Output Set: N:\CRF3\06052002\J019541.raw

ENTERED

4 <110> APPLICANT: Herbers, Karin
 5 Badur, Ralf
 6 Kunze, Irene
 7 Geiger, Michael
 8 Mock, Hans-Peter

10 <120> TITLE OF INVENTION: Identification and overexpression of a DNA sequence encoding
 a 2-methyl-6-phytylhydroquinone methyltransferase in
 11 plants.
 12

14 <130> FILE REFERENCE: 0817/00001
 16 <140> CURRENT APPLICATION NUMBER: US 10/019,541
 C--> 17 <141> CURRENT FILING DATE: 2002-05-06
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP/00/05862
 18 <151> PRIOR FILING DATE: 2000-06-23
 20 <160> NUMBER OF SEQ ID NOS: 10
 22 <170> SOFTWARE: WordPerfect version 6.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 957
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Synechocystis PCC6803
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(957)
 33 <400> SEQUENCE: 1

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37	1 5 10 15	
39	gcg atc gcc gct gga ctg tat ctc cta act gcc cgg ggc tat cag tca	96
40	Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser	
41	20 25 30	
42	tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac ggc att	144
43	Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile	
44	35 40 45	
46	ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat ggc gat	192
47	Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp	
48	50 55 60	
50	ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt gtc cat	240
51	Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His	
52	65 70 75 80	
54	gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc aca acg	288
55	Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr	
56	85 90 95	
58	gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc gcc	336
59	Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala	

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60          100          105          110
62 aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc caa cag 384
63 Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
64          115          120          125
66 gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc aag ttt 432
67 Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
68          130          135          140
70 gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc gac 480
71 Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
72 145          150          155          160
74 gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa gct gtg 528
75 Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
76          165          170          175
78 ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att ctg gtg 576
79 Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
80          180          185          190
82 gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac ttc 624
83 Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
84          195          200          205
86 tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc cac cct 672
87 Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
88          210          215          220
90 gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc acg ggt 720
91 Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
92 225          230          235          240
94 ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg acc ctc 768
95 Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
96          245          250          255
98 ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc cag ggc 816
99 Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
100          260          265          270
102 tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg gaa gta 864
103 Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
104          275          280          285
106 ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt cgc 912
107 Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
108          290          295          300
110 ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct taa 957
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112 305          310          315
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115 <211> LENGTH: 318
116 <212> TYPE: PRT
117 <213> ORGANISM: Synechocystis PCC6803
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124 Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser
125          20          25          30

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127 Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile
128          35          40          45
130 Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
131          50          55          60
133 Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
134 65          70          75          80
136 Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
137          85          90          95
139 Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
140          100          105          110
142 Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
143          115          120          125
145 Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
146          130          135          140
148 Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
149 145          150          155          160
151 Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
152          165          170          175
154 Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
155          180          185          190
157 Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
158          195          200          205
160 Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
161          210          215          220
163 Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
164 225          230          235          240
166 Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
167          245          250          255
169 Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
170          260          265          270
172 Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
173          275          280          285
175 Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
176          290          295          300
178 Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
179 305          310          315

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181 <210> SEQ ID NO: 3

182 <211> LENGTH: 974

183 <212> TYPE: DNA

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186 <220> FEATURE:

187 <221> NAME/KEY: CDS

188 <222> LOCATION: (7)..(963)

190 <400> SEQUENCE: 3

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194      1          5          10
196 tcc ctg gcg atc gcc gct gga ctg tat ctc cta act gcc cgg ggc tat      96
197 Ser Leu Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr

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202		35		40		45		
204	ggc att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat	192						
205	Gly Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr							
206		50		55		60		
208	ggc gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt	240						
209	Gly Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe							
210		65		70		75		
212	gtc cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc	288						
213	Val His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly							
214		80		85		90		
216	aca acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att	336						
217	Thr Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile							
218		95		100		105		110
220	ctc gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc	384						
221	Leu Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro							
222		115		120		125		
224	caa cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc	432						
225	Gln Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala							
226		130		135		140		
228	aag ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt	480						
229	Lys Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser							
230		145		150		155		
232	ttc gac gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa	528						
233	Phe Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys							
234		160		165		170		
236	gct gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att	576						
237	Ala Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile							
238		175		180		185		190
240	ctg gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc	624						
241	Leu Val Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu							
242		195		200		205		
244	aac ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc	672						
245	Asn Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser							
246		210		215		220		
248	cac cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc	720						
249	His Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala							
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252	acg ggt ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg	768						
253	Thr Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro							
254		240		245		250		
256	acc ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc	816						
257	Thr Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro							
258		255		260		265		270
260	cag ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg	864						
261	Gln Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg							
262		275		280		285		

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264 gaa gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt 912
265 Glu Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu
266          290          295          300
268 tgt cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct 960
269 Cys Arg Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
270          305          310          315
272 taa attgcggatc c 974
275 <210> SEQ ID NO: 4
276 <211> LENGTH: 318
277 <212> TYPE: PRT
278 <213> ORGANISM: Synechocystis PCC6803
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286 20 25 30
288 Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile
289 35 40 45
291 Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
292 50 55 60
294 Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
295 65 70 75 80
297 Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
298 85 90 95
300 Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
301 100 105 110
303 Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
304 115 120 125
306 Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
307 130 135 140
309 Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
310 145 150 155 160
312 Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
313 165 170 175
315 Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
316 180 185 190
318 Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
319 195 200 205
321 Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
322 210 215 220
324 Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
325 225 230 235 240
327 Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
328 245 250 255
330 Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
331 260 265 270
333 Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
334 275 280 285
336 Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg

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VERIFICATION SUMMARY

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Input Set : A:\019541

Output Set: N:\CRF3\06052002\J019541.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date